



SEQUENCE LISTING

<110> McCarthy, Sean A.

<120> NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR

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<150> 08/842,898

<151> 1997-04-17

<150> 60/071,589

<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
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Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
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Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
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Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
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gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac 295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn
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Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	
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Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
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acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca	439
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tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac	487
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Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
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Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
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Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
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35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
100 105 110
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
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Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
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Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
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Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
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Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
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tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe 275 280 285	864
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aagg atg gtg gcg gcc gtc ctg ctg ggg ctg agc tgg ctc tgc tct ccc 169
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Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp
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Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys
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aat acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt 313
Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys
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Ala Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys
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tgc cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat 409
Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp
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Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His
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gca gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg 505
Ala Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg
              115              120              125
aag cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa 553
Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu
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 His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val
 160 165 170 175

tgc tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc 697
 Cys Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe
 180 185 190

cag cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc 745
 Gln Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr
 195 200 205

agc aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag 793
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Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
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Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
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Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
 100 105 110

Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
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Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
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Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145 150 155 160

Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
165 170 175

Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
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Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
20 25 30

cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc aat 144
His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
35 40 45

acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt gct 192
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
50 55 60

aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc tgc 240
Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
65 70 75 80

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Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
85 90 95

acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat gca 336
Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
100 105 110

gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg aag 384
Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
115 120 125

cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa agt 432
Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
130 135 140

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Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145 150 155 160

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Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
165 170 175

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Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
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195 200 205

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Met Met Ala Leu Gly Ala Ala
1 5

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Gly Ala Thr Arg Val Phe Val Ala Met Val Ala Ala Ala Leu Gly Gly
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His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser Val Leu Asn Ser
25 30 35

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Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly Ala Ala Gly His
40 45 50 55

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Pro Gly Ser Ala Val Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly
60 65 70

aat aag tac cag acc att gac aac tac cag ccg tac ccg tgc gca gag 353
 Asn Lys Tyr Gln Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu
 75 80 85

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gaa acc atc act gaa agc ttt ggt aat gat cat agc acc ttg gat ggg 593
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 170 175 180

caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt gcc tca gga ttg 689
 Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ser Gly Leu
 185 190 195

tgt tgt gct aga cac ttc tgg tcc aag atc tgt aaa cct gtc ctg aaa 737
 Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Lys
 200 205 210 215

gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc tct cat gga cta 785
 Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu
 220 225 230

gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg tct tgc cgg ata 833
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<210> 8
<211> 266
<212> PRT
<213> Homo sapiens

<400> 8
Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
1 5 10 15
Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
20 25 30
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
35 40 45
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
50 55 60
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
65 70 75 80
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
85 90 95
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
100 105 110
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
115 120 125
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
130 135 140
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
145 150 155 160
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
165 170 175

Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
180 185 190
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
195 200 205
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
210 215 220
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
225 230 235 240
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
245 250 255
Ser Ser Arg Leu His Thr Cys Gln Arg His
260 265

<210> 9
<211> 798
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(798)

<400> 9
atg atg gct ctg ggc gca gcg gga gct acc cgg gtc ttt gtc gcg atg 48
Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
1 5 10 15
gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc 96
Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
20 25 30
ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg 144
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
35 40 45
ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg 192
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
50 55 60
gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac 240
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
65 70 75 80
cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac 288
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
85 90 95
tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc 336
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
100 105 110

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gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc   384
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
      115                      120                      125

ccc ggg aat tac tgc aaa aat gga ata tgc gtg tct tct gat caa aat   432
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
      130                      135                      140

cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat   480
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
      145                      150                      155                      160

gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca   528
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
      165                      170                      175

aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca   576
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
      180                      185                      190

tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag   624
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
      195                      200                      205

atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg   672
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
      210                      215                      220

aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga   720
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
      225                      230                      235                      240

gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat   768
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
      245                      250                      255

tct tct agg ctt cac act tgt cag aga cac                               798
Ser Ser Arg Leu His Thr Cys Gln Arg His
      260                      265

<210> 10
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(537)

<400> 10
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga   48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
      1                      5                      10                      15

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tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
          20          25          30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
          35          40          45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
          50          55          60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
          65          70          75          80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
          85          90          95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
          100          105          110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
          115          120          125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
          130          135          140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
          145          150          155          160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
          165          170          175

cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa 577
Gln Lys Ile

gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637

taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg 697

gccgc 702

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<210> 11
<211> 179
<212> PRT
<213> Homo sapiens

<400> 11

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Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1 5 10 15
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30
 Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
 35 40 45
 Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
 50 55 60
 Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65 70 75 80
 Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
 85 90 95
 Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
 100 105 110
 Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
 115 120 125
 His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
 130 135 140
 Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 145 150 155 160
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
 165 170 175
 Gln Lys Ile

<210> 12
 <211> 537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (537)

<400> 12
 gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
 Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1 5 10 15
 tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30

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gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
      35              40              45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
      50              55              60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
      65              70              75              80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
      85              90              95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
      100              105              110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
      115              120              125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
      130              135              140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
      145              150              155              160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
      165              170              175

cag aaa att
Gln Lys Ile

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537

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<210> 13
<211> 928
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (75)..(800)

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<400> 13
ctcgaggcca aaattcggca cgaggccggg ctgtggtcta gcataaaggc ggagcccaga 60

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agaaggggac gggg atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg 110
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg
      1              5              10

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cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc	158
His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser	
15 20 25	
gct gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt	206
Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly	
30 35 40	
ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg	254
Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu	
45 50 55 60	
aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg	302
Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met	
65 70 75	
gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag	350
Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu	
80 85 90	
cac cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag	398
His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys	
95 100 105	
atg acc gac aac aag aca gga gag gtg ctg atc tcc gag aat gtg gtg	446
Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val	
110 115 120	
gca tcc att caa cca gcg gag ggg agc ttc gag ggt gat ttg aag gta	494
Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val	
125 130 135 140	
ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg	542
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr	
145 150 155	
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att	590
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile	
160 165 170	
aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac	638
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His	
175 180 185	
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc	686
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu	
190 195 200	
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc	734
Arg Lys Gly Thr His Lys Asp Val Leu Glu Gly Thr Glu Ser Ser	
205 210 215 220	
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc	782
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu	
225 230 235	

agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 830
Arg Pro Ser Arg Gln Leu
240

tagcccccacat cagaccctgc cccaagcacc atatggaaat aaagttcttt cttacatcta 890

aaaaaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc 928

<210> 14
<211> 242
<212> PRT
<213> Homo sapiens

<400> 14
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1 5 10 15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
50 55 60
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65 70 75 80
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
165 170 175
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
180 185 190
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
195 200 205
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
210 215 220

Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
 225 230 235 240

Gln Leu

<210> 15
 <211> 726
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (726)

<400> 15
 atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat ctg ctg gtc 48
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 1 5 10 15
 ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct 96
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 20 25 30
 atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc 144
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 35 40 45
 cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg 192
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 50 55 60
 ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc 240
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 65 70 75 80
 ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg 288
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 85 90 95
 aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac 336
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
 100 105 110
 aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa 384
 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
 115 120 125
 cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag 432
 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
 130 135 140
 gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac 480
 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
 145 150 155 160

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aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg 528
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
      165                      170                      175

cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag 576
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
      180                      185                      190

aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc 624
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
      195                      200                      205

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg 672
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
      210                      215                      220

ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg 720
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
      225                      230                      235                      240

cag ctg
Gln Leu
                                                    726

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<210> 16
<211> 2381
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (110)..(1156)

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<400> 16
mgtcgaccca cgcgtccgct gtggcagccc agctaccggt cgtgaccaga tccagcttgc 60

agctcagctt tgttcattcg aattgggcgg cggccagcgc ggaacaaac atg cag cgg 118
                                                    Met Gln Arg
                                                    1

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ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act 166
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr
      5                      10                      15

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc 214
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly
      20                      25                      30                      35

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt 262
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe
      40                      45                      50

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt 310
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser
      55                      60                      65

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gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct	358
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys Thr Ser Ser	
70 75 80	
gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc	406
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser	
85 90 95	
acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt	454
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val	
100 105 110 115	
cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca	502
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr	
120 125 130	
gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt	550
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys	
135 140 145	
atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc	598
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser	
150 155 160	
ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc	646
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr	
165 170 175	
cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc	694
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys	
180 185 190 195	
acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag	742
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln	
200 205 210	
agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg	790
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu	
215 220 225	
ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac	838
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp	
230 235 240	
ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa	886
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu	
245 250 255	
gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca	934
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro	
260 265 270 275	
cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc	982
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser	
280 285 290	

cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag 1030
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu
295 300 305

tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac 1078
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp
310 315 320

ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct 1126
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro
325 330 335

gtg gag tca cta ggc gga gag gag gag att taggccaga cccagctgag 1176
Val Glu Ser Leu Gly Gly Glu Glu Ile
340 345

tcactggtag atgtgcaata gaaatggcta atttattttc ccaggagtgt cccaagtgt 1236

ggaatggccg cagctccttc ccagtagctt ttctctggc ttgacaaggt acagtgcagt 1296

acatttcttc cagccgccct gcttctctga cttgggaaag acaggcatgg cgggtaaggg 1356

cagcggtag tgcctcctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag 1416

atttgtttga agggagagga tgggaagggg tgaagtctgc tcatgatgga tttgggggat 1476

acagggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgccttt 1536

gtcttgccgc gctcccatgg gctgaggcag tggctacaca agagctatgc tgctctgttg 1596

cctcccatc attcatccct gtgtttcagc tctacctca ctgtcagcac agcccttcat 1656

agccacgccc cctcttgctc accacagcct aggaggggac cagaggggac ttctctcaga 1716

gccccatgct ctctctctca accccatacc agcctctgtg ccagcgacag tccttccaaa 1776

tggagggagt gaaatccttt ggtttaatta ttttctcctt caaggcacgc ctgccactaa 1836

ggtcaggctg acttgcatgt ccctctaacg ttcttagcag tgtggtggac actgtcttcc 1896

accgactgct tcaatacctc tgaaagccag tgctcggagt gcagttcgtg taaattaatt 1956

tgcaggaagt atacttggct aattgtaggg ctaggattgt gaatgaaatt tgcaaagtcg 2016

cttagcaaca atggaaagcc tttctcagtc acaccgagaa gtcacaacca agccaggttg 2076

tgtagagtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggcctcaga 2136

tgacggtttc aggtgccagg aactattacc attctgtatc tatccagagt tattaataatt 2196

gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2256

acaaacatgt ggcctcaaa gatcatgcac aaaccactac tctttgctaa ttcttggaact 2316

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<212> PRT
<213> Homo sapiens

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Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145 150 155 160
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
180 185 190
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
 275 280 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
 290 295 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
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Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
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gtc ccc act gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg 96
 Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
 20 25 30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat 144
 Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 35 40 45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa 192
 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 50 55 60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa 240
 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys
 65 70 75 80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat 288
 Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
 85 90 95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac 336
 Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
 100 105 110

cag gaa gtt cac aag ata acc aac aac cag agt gga cag gtg gtc ttt	384
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe	
115 120 125	
tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc	432
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser	
130 135 140	
cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag	480
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln	
145 150 155 160	
ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg	528
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met	
165 170 175	
cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg	576
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp	
180 185 190	
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Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys	
195 200 205	
gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga	672
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg	
210 215 220	
ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc	720
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu	
225 230 235 240	
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Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu	
245 250 255	
gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta	816
Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu	
260 265 270	
tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc	864
Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe	
275 280 285	
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Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala	
290 295 300	
ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag	960
Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu	
305 310 315 320	
ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg	1008
Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly	
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340 345

1047

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